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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(EC
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alpha-globulin B precursor (clone C72) - upland cotton N; Alternate names: seed storage protein; vicilin precursor C; Species: Gossyplum hirsutum (upland cotton) C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_c) C; Accession: A30838; S06911 R; Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A; Title: Developmental biochemistry of cottonseed embryoger A; Reference number: A30838 RESULT FWCNAB 뫄 Qy DЬ C;Superfamily: glycinin C;Keywords: seed; storage protein F;1-24/Domain: signal sequence #status A; Title: Comparison of the structure and nucleotide A; Reference number: S22477; MUID:92288309 A; Accession: S22477 vicilin precursor - cacao (cacao) C:Species: Theobroma cacao (cacao) C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 C:Accession: S22477; S22478; S18105; S22050 A; Molecule type: mRNA A; Introns: 211/1; 269/3; 296/3; 391/3; 502/1 C; Genetics: A; Molecule type: mRNA A; Residues: 1-452 < MC2> A, Cross-references: EMBL:X62625 A, Accession: S22478 A; Molecule type: DNA A; Residues: 1-566 <MCH> R:MCHenry, L.; Fritz, P.J. Plant Mol. Biol. 18, 1173-1176, 1992 F;25-566/Product: vicilin #status predicted A; Cross-references: EMBL: X62626 Query Match 44.8 Best Local Similarity 31.4 Matches 32; Conservative 95 47 35 QQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEE 136 -----EERMKEED 68 ERDPRQQYEQCQRRCESEATEEREQEQCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQE 44.8%; 20; Score 172; DB Pred. No. 2.6e 20; Mismatches of cottonseed embryogenesis and germination XVIII predicted icted <MAT> 30-Sep-1991 #text_change 16-Jul-1999 DB 2; .6e-07; <SIG> #text_change sequence Length 566; Indels of. 36; vicilin genes of coco 17-Mar-1999 Gaps 94 46 2

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A; Molecule type: DNA
A; Residues: 1-509 < CHL>
C; Superfamily: alvaini
                 Plant
                                                                             C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
                                                                                                                                                                    RESULT
S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar
C:Accession: S08059
                                                                                                                       N; Alternate names: seed storage protein
                                                                                                                                             alpha-globulin type A precursor - upland cotton
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Plant Mol. Biol.
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A; Residues: 1-81 <CH2>
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A; Accession: S06911
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                                        R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III,
                                                              C; Accession: S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with
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A; Residues: 1-588 <CHL>
A; Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Developmental biochemistry of cottonseed embryogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: glycinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comment: This is a seed storage protein
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                       Mol.
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                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      1 NRQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQ------
Developmental
                                                                                                                                                                                                                                                        KKQQCVRECREKYQENPWRGEREEEAEEEE
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                                                                                                                                                                                                                                                                                              -----REDEEKY-----
                                                                                                                                                                                                                                                                                                                                     DPQRRYEECQQEC---RQQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRPEDPQRRYEECQQEC -- RQQEERQRPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQE 135
                       Biol. 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borroto, K.; Kamalay, J.A.; Dure III,
l. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -REDEEKYEE----RMKEED 68
                       533-546,
biochemistry of cottonseed
                                                                                                                                                                                                                                                                                                                                                                                                                                     38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conceptual translation
                       1987
                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                              -EERMKEED 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147; DB 2;
Pred. No. 2.6e-05;
17; Mismatches 14
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
embryogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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germination.
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XIX.
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BB
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A; Kesidues: 1-1038 <RIE>
A; Cross-references: EMBL:AF000580; NID:g3068582; PIDN:AAC14390.1; A; Experimental source: strain WS2162
C; Genetics:
                                                                                                                                                                                     protein PV100 [imported] - winter squash
C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status
F;25-605/Product: alpha-globulin type /
A; Molecule type: mRNA
A; Residues: 1-810 < YAM>
                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                          J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are A;Reference number: Z22767; MUID:99107919
A;Accession: T44430
                                                                                                                                              R; Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura,
                                                                                                                                                                    C; Accession: T44430
                                                                                                                                                                                                                                                        T44430
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A; Mobile element:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z14684; MUID:98198836
A;Accession: T02634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, H.; H
Genetics 148, 1117–1125, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rep protein homolog - slime mold (Dictyostelium discoideum) plasmid Ddp5 C;Species: Dictyostelium discoideum C;Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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Best Local Similarity
Tatches 29; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-605 < CHL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S06398
A; Accession: S06398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T02634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 KQQ--KRYEEQQRED-----EEKYEERMKEEDN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQ-QREDEEKYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQQCVKECREQYQEDPWKGERENKWREEEEEESD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQRRYQDCRQHCQQEERRLRPHCEQSCREQYEKQQQQQPDKQFKECQQRCQWQEQRPER 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid Ddp5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             status predicted <SIG>
type A #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 116.5; DB Pred. No. 0.014;
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Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                     produced
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                                                                                                       Asn-Gln bonds
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A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062

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hypothetical protein 1 - African malaria mosquito (fragment)
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: $27770
C;Accession: $27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
submitted to the EMBL Data Library, June 1992
A;Description: Distinct families of site-specific retroposons occupy identic A;Reference number: $27770
A;Reference number: $27770
A;Recession: $27770
A;Residues: 1-613 <BES>
A;Cross-references: EMBL:M93690; NID:g159615; PID:g159616
                                                                                                                                                                                                                                                                                                                                                                                                             R:Geissler, H.; Schwarz, E.C.; Soldati, T. submitted to GenBank, September 1998
A:Description: Identification of two novel and highly divergent myosins in Dictyostelium
                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-1737 <CEII>
A;Cross-references: GB:AF090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714396
A;Experimental source: strain AX2
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unconventional myosin heavy chain MyoM - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Species: Dictyostelium discoideum
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59235
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A59235
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                           δõ
                                                                                                                                                                  C; Superfamily: myosin motor domain homology F:62-874/Domain: myosin motor domain homology #status atypical <MMO>
                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A59235
A; Accession: A59235
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                                                                                                                                                                                                          A; Map position: 6, aldB-cabA2
                                                                                                                                                                                                                                    A;Gene: myoM
                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; not compared with conceptual translation
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                                                                Query Match
Best Local S
Matches 25
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 18; Conser
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NRORDPOQQYEQCOKHCORRETEPRHMQTCQORCERRYEKE-KRKQOKRYEEQQREDEEK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RORDPOOQYEQCOKHCORRETEPRHMQTCOQRCERRYEKEKRKQOKRYEEQQREDEEKYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REEQRRREHEREERRRERE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEEQQREDEEKYEERMKEED 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQRGSPRAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVDEVERRDPEWE 128
                                                                27.3%; Solution 27.3%; Solution 27.3%; P. 25; Conservative 20;
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                                                             Score 105; DB:
Pred. No. 0.19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 2; Pred. No. 0.081;
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                                                                                                        Length 1737;
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                                                                Indels
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trfA protein - slime mold (Dictyosteliu
C;Speciaes: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T14004
R;Saito, J.; Adachi, H.; Sutoh, K.
J. Biol. Chem. 273, 24654-24659, 1998
                                                                                                                                                                                                                                                                     A;Title: Dictyostelium TRFA homologous to yeast Ssn6 is A;Reference number: Z17852; MUID:98406112 A;Accession: T14004 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1390 <SAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:C11G6.3
A;Map position: X
A;Introns: 12/1; 106/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z70204; PIDN:CAA94113.1; GSPDB:GN000028; CESP:C11G6. A;Experimental source: clone C11G6 C;Genetics:
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A;Accession: T19201
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-385 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C11G6.3 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T19201 R;Wilkinson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: Z19089
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                                                                                                                                                                                       A; Introns:
                                                                                                                                                                                                               A;Gene: trfA
                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AB009080; NID:d1228566; PID:d1034109; PIDN:BAA33143.1
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                                                                                Query Match 27.1%;
Best Local Similarity 23.9%;
Matches 16; Conservative 3
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Best Local
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Local Similarity
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                                  2 RORDPOQOYEOCOKHCORKETEPRHMOTCOORCERRYEKEKRKOOKRYEEOOREDEEKYE 61
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27.6%;
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                                                                                  30;
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                                                                                Score 104; DB Pred. No. 0.19; 0; Mismatches
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                                                                                                                         Length 1390;
                                                                                  Indels
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151 QQQQQQD 157

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1407 <FIE>
A;Cross-references: EMBL:219092; NID:91746; PIDN:CAA79519.1; PID:91747
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root Covalent modifications to this protein include conversion of arginine to citrulline an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fietz, M.J.; Rogers, G.E. submitted to the EMBL Data Library, December 1992 submitted to the EMBL Data Library, December 1992 recording rabbit trichohyaling the gene encoding the gene encodi
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C;Date: 12-Mar-1993 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
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C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>
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A:Residues: 1-1898 <-KEEP>
A:Residues: 1-1898 <-KEEP>
A:Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A:Note: authors translated the codon AGG for residue 1714 as Pro
C:Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she covalent modifications to this protein include conversion of arginine to citrulline and
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C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
C;Accession: A45973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steine:
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A;Tille: The structure of human trichohyalin. Potential multiple roles as a function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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                                                                                                                                                                                                Score 102; DB 1;
Pred. No. 0.28;
0; Mismatches 19
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Pred. No. 0.26;
9; Mismatches
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   R; Su, Y
EMBO J.
                                                            C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
C;Accession: T30989
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C;Species: Homo sapiens (man)
C;Date: (04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C;Accession: T46401
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17218
                                                                                                                                                           serine/threonine protein kinase NIK - mouse N;Alternate names: Nck interacting kinase
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A; Residues: 1-1027 < AAA>
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A;Residues: 1-233 <POU>
A;Cross-references: EMBL:AL117408
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A; Accession: T17218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein DKFZp434P1750.1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein DKFZp434A025.1 - human (fragment)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
   Y.C.;
J. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 RQKRIEQQKEQRRRLEEQQRREEREARRQQEREQR---RREQEEKRRLEELERRRKEEEEERR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 KETRKQEKERQKQEKERQKQEKEREKERQKQEKEREKQEKERQKQE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 EQEERREQRLEQEE 327
                                                                                                                                                                                                                                                                                                                                                               192 RAEEEKRRVEREQEYIRRQLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                               55 -----EDEEKYEERMKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 KHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 35.1
les: 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RQRDPQQQYEQCQK -- HCQRRETEPRHMQTCQQRCERRYEKEKRK ---- QQKRYEEQQR- 54
Han, J.; Xu, S.;
1279-1290, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.3%;
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                                 Cobb, M.; Skolnik, E.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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Pred. No. 0.08;
8; Mismatches
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Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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A;Title: NIK is a new Ste20-related kinase that binds NCK and MEKK1 and activates the SA A;Reference number: Z20954; MUID:97280817
A;Accession: T30989
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1233 <SUY>
A;Cross-references: EMBL:U88984; NID:g1872545; PID:g1872546; PIDN:AAC53165.1
C;Keywords: protein kinase
                                                                                                                                                                                                                                                 ₽
Search completed: March 1, 2001, 15:52:21 Job time: 545 sec
                                                                                                                                                                                                                                                                                                                                                    Query Match 26.3%; Score 101; DB 2; Length 1233; Best Local Similarity 36.1%; Pred. No. 0.3; Matches 30; Conservative 16; Mismatches 19; Indels 18
                                                                                                                                                                                                                                           452 RAEEEKRRVEREQEYIRRQLEEE 474
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